

## scFv(UCHT-1)-PE38

single chain Fv fragment



# amino acid residues:	109	16	122	5	347
------------------------	-----	----	-----	---	-----

$V_L$ =light chain variable region

L = peptide linker (GGGS)4

$V_H$ =heavy chain variable region

C = connector segment (KASGG)

Toxin = PE38 fragment of *Pseudomonas aeruginosa* exotoxin A

FIG.1

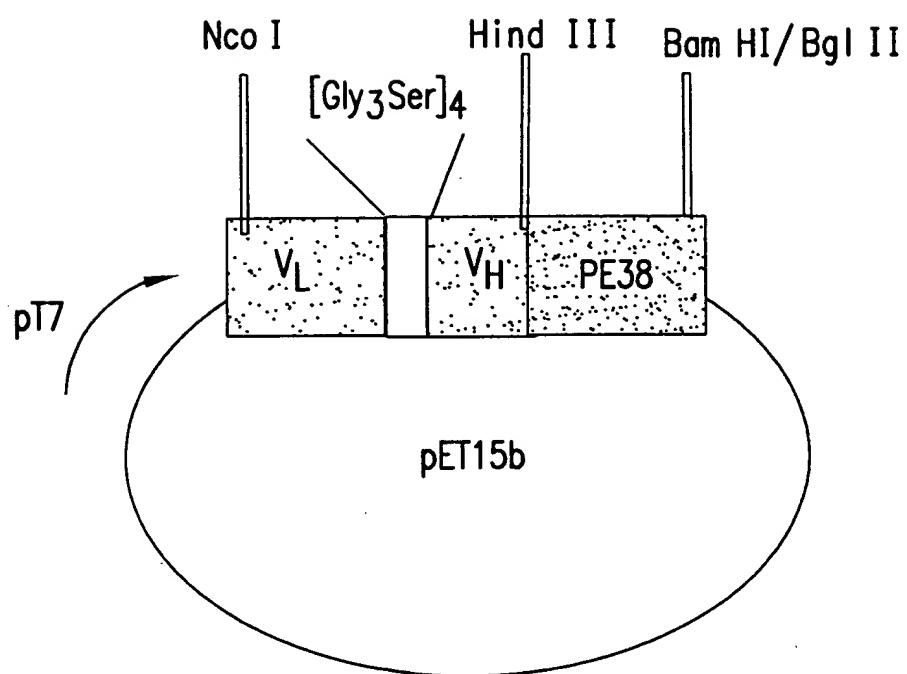


FIG.2

3/23

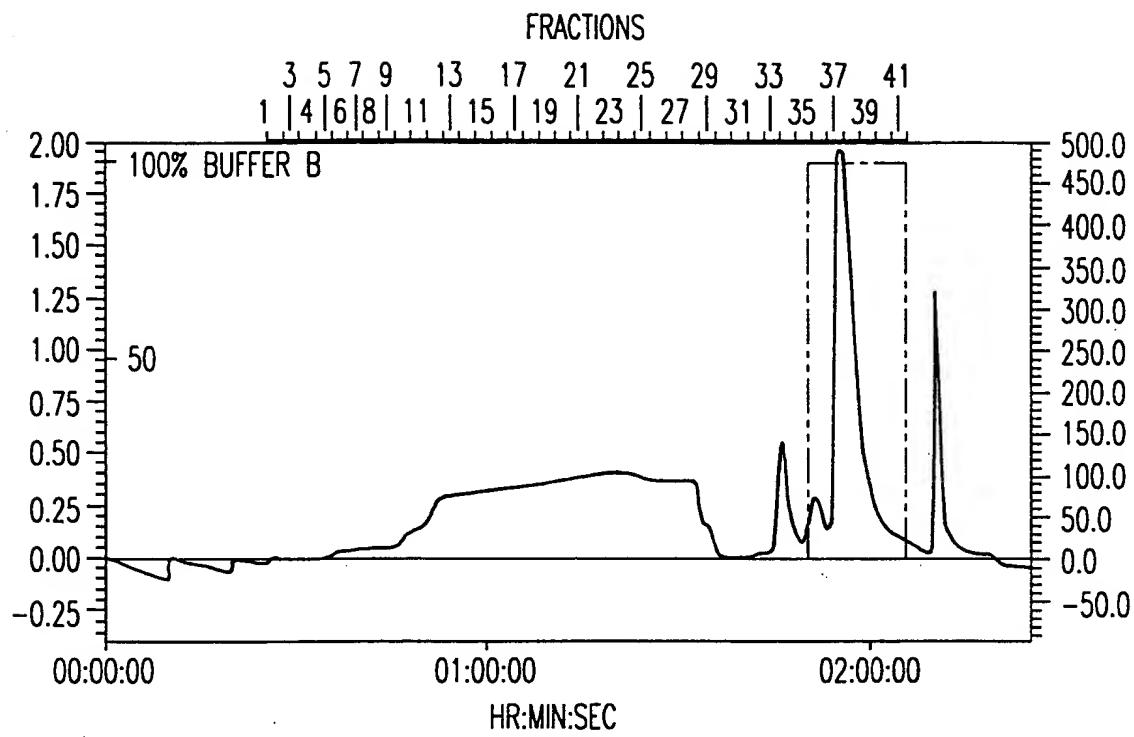


FIG. 3A

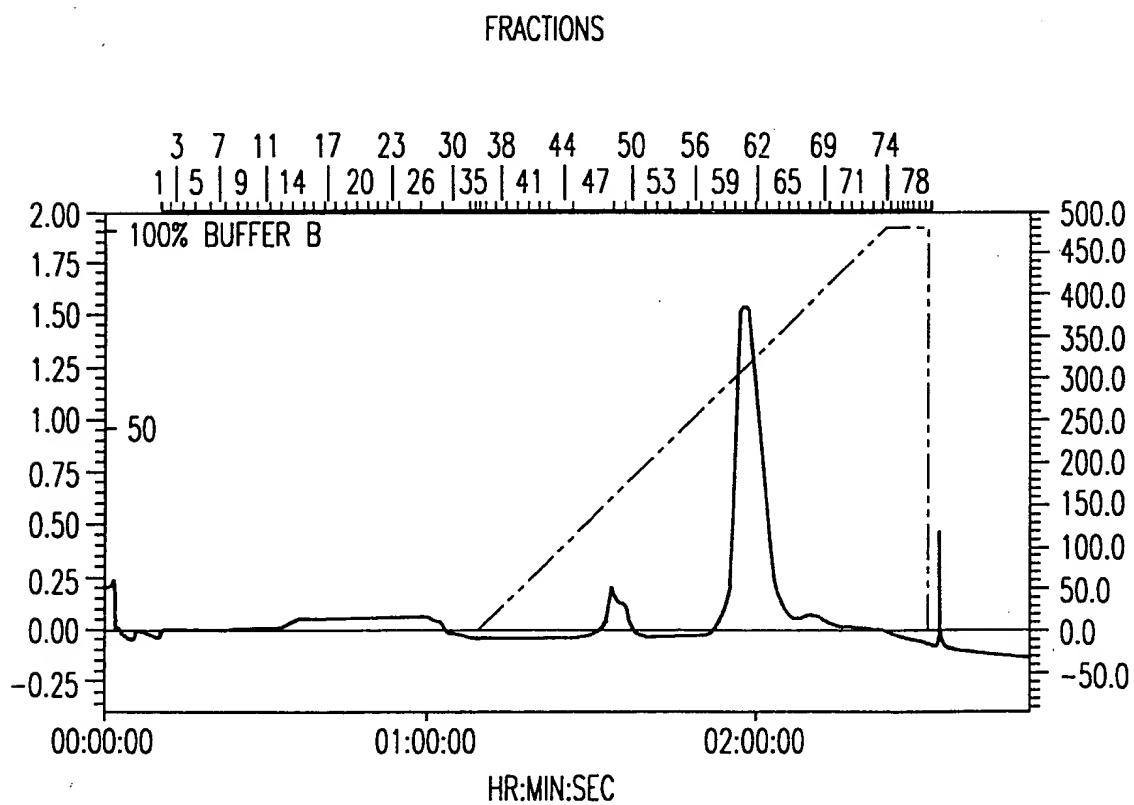


FIG. 3B

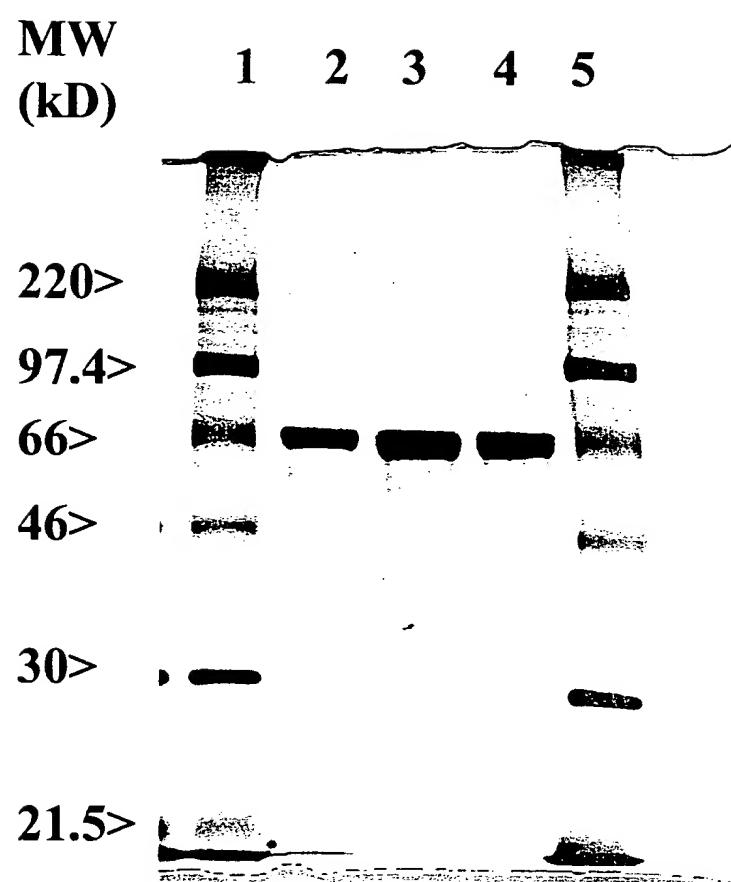


FIG.4

5/23

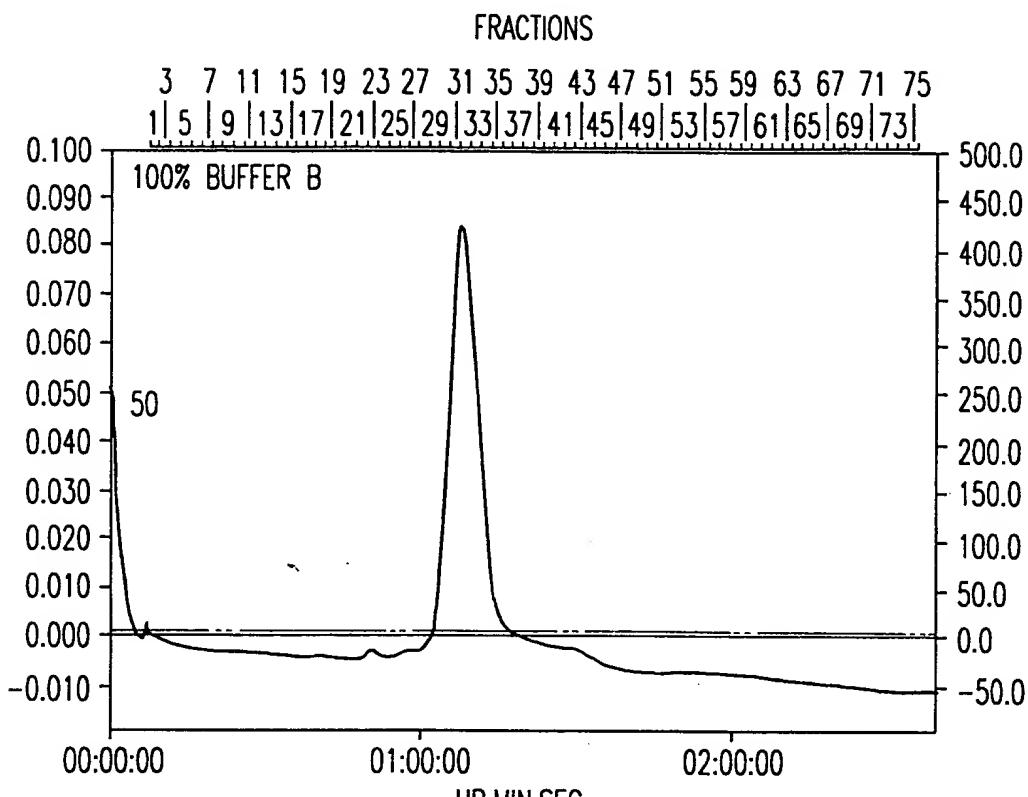


FIG. 5A

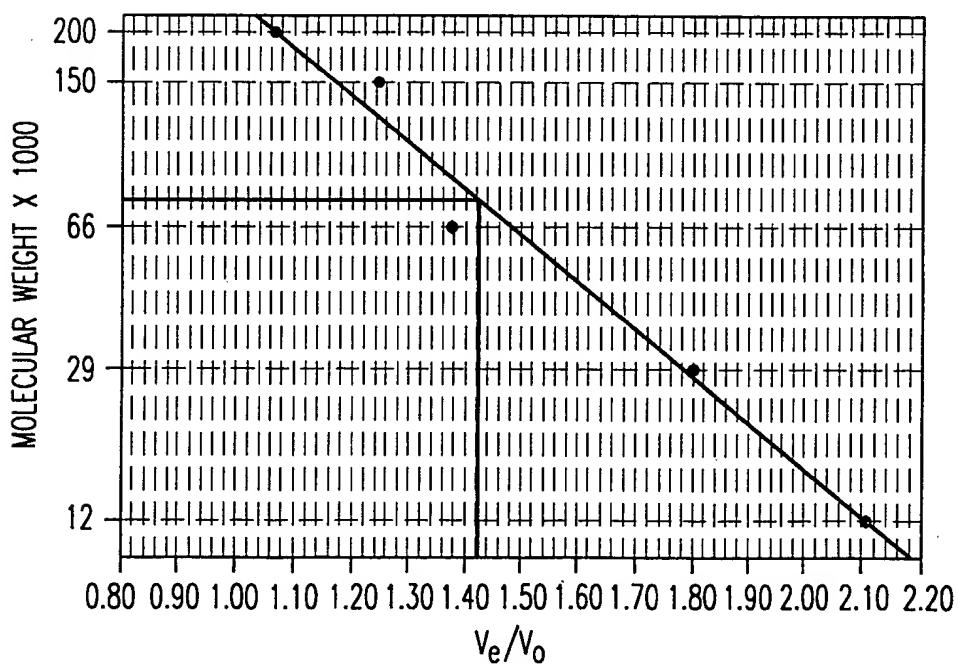


FIG. 5B

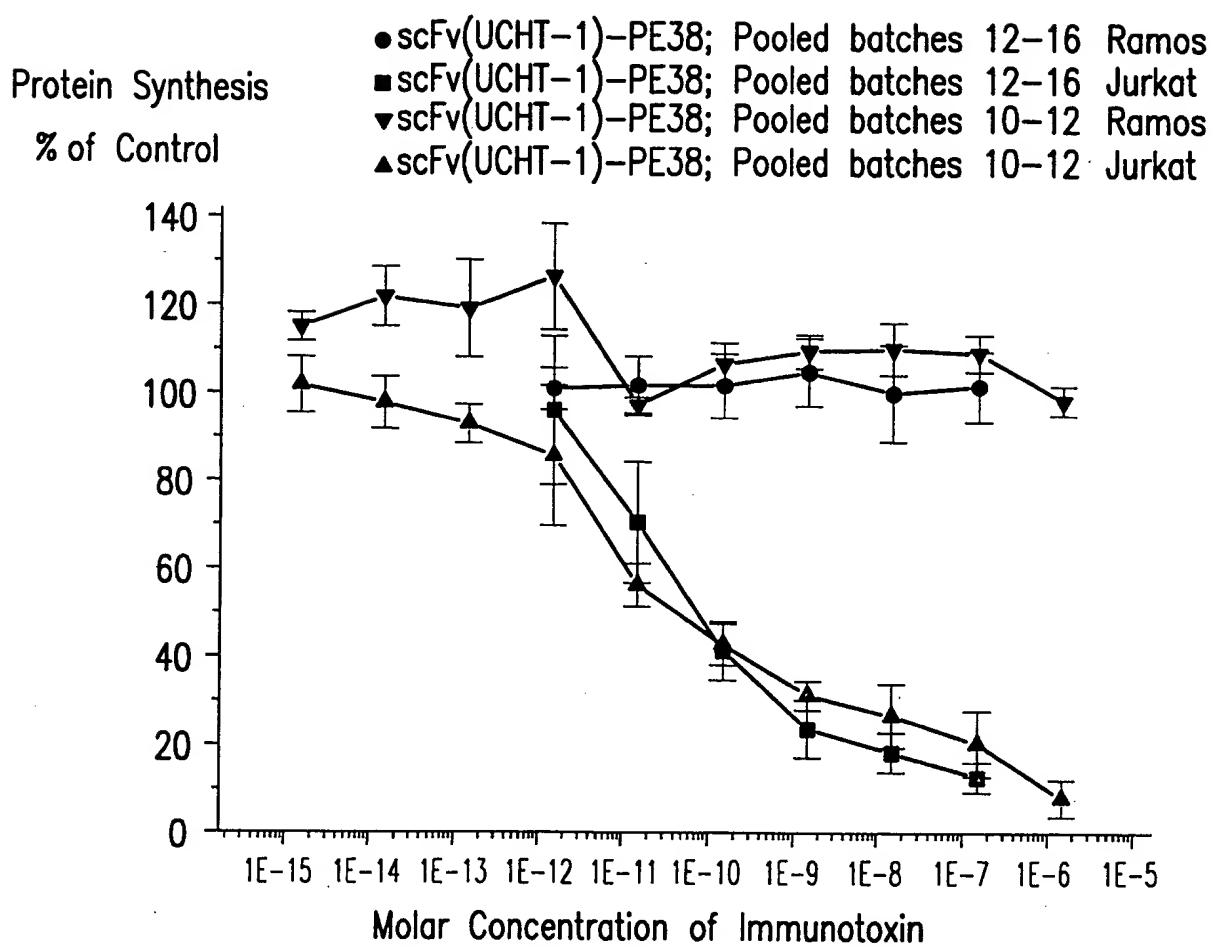


FIG.6

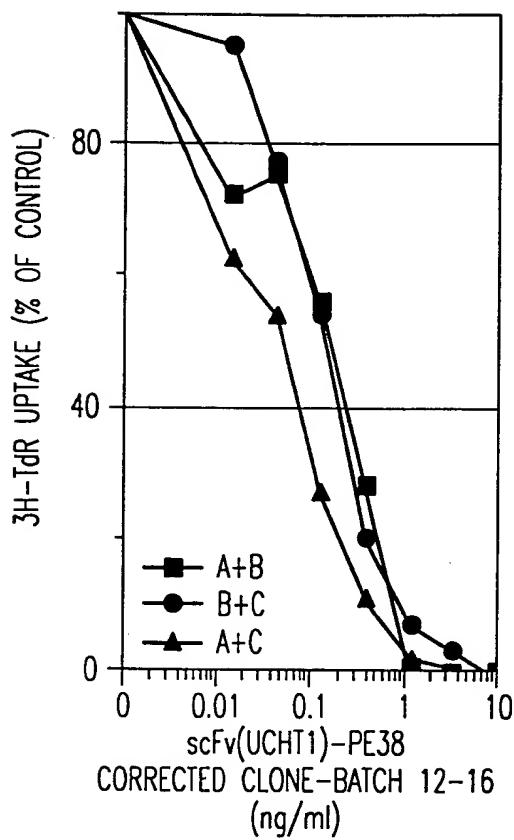


FIG. 7A

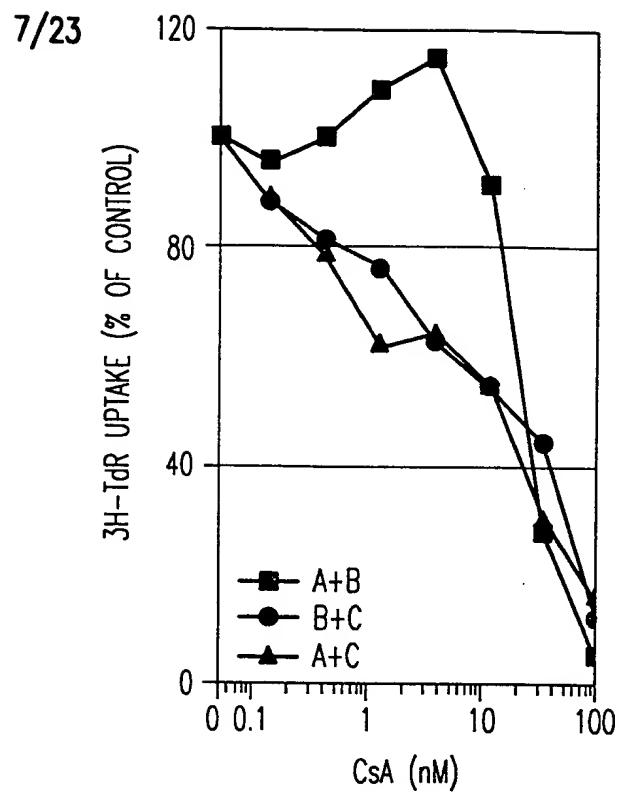


FIG. 7B

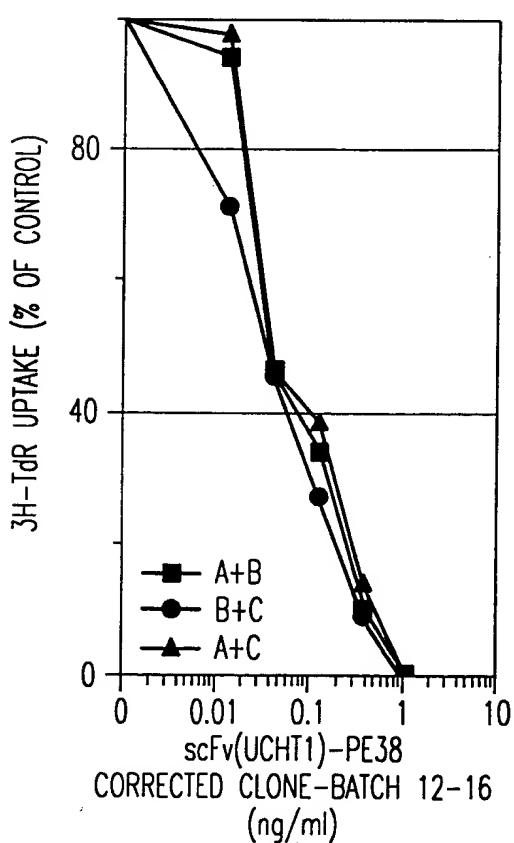


FIG. 7C

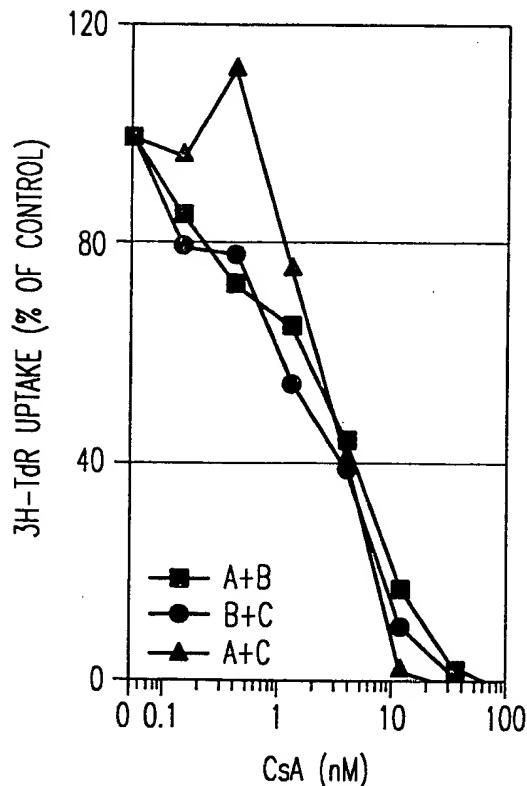


FIG. 7D

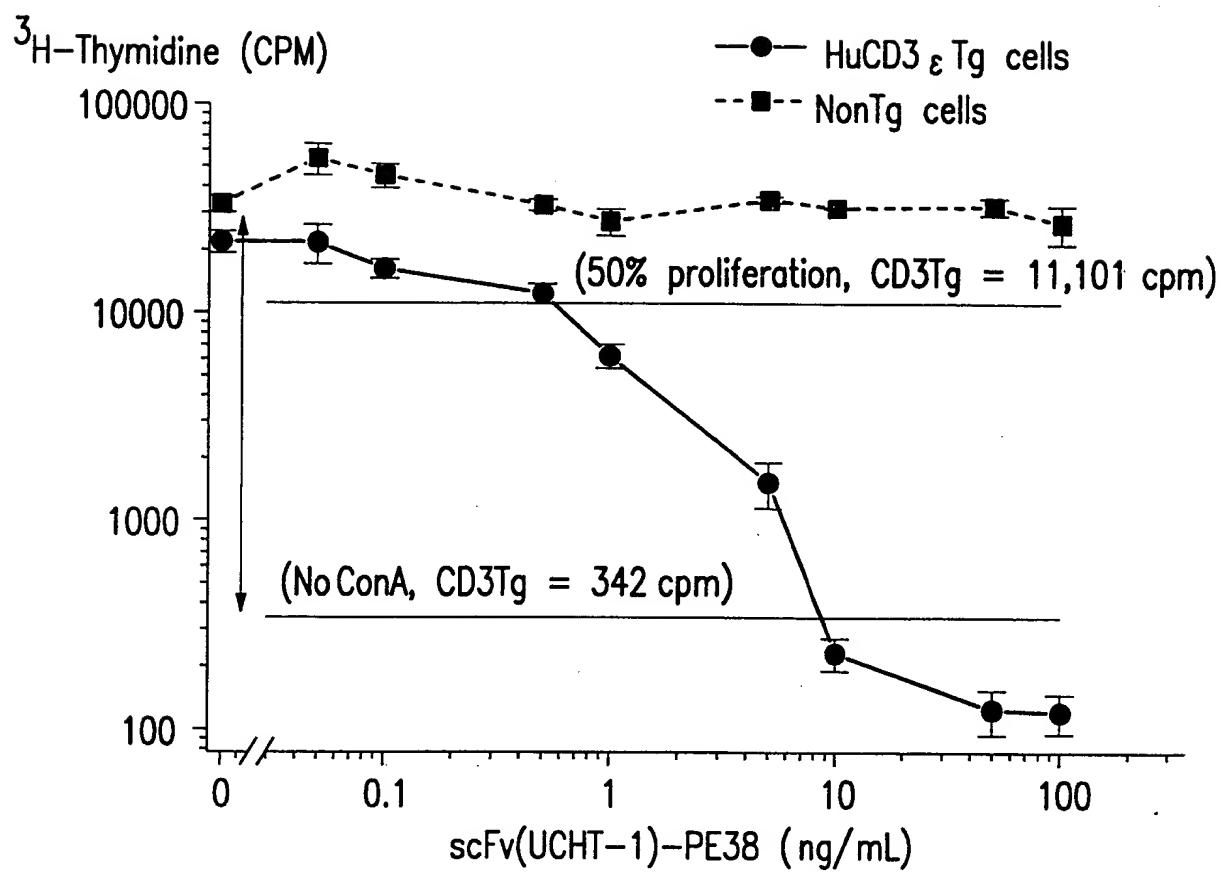


FIG.8

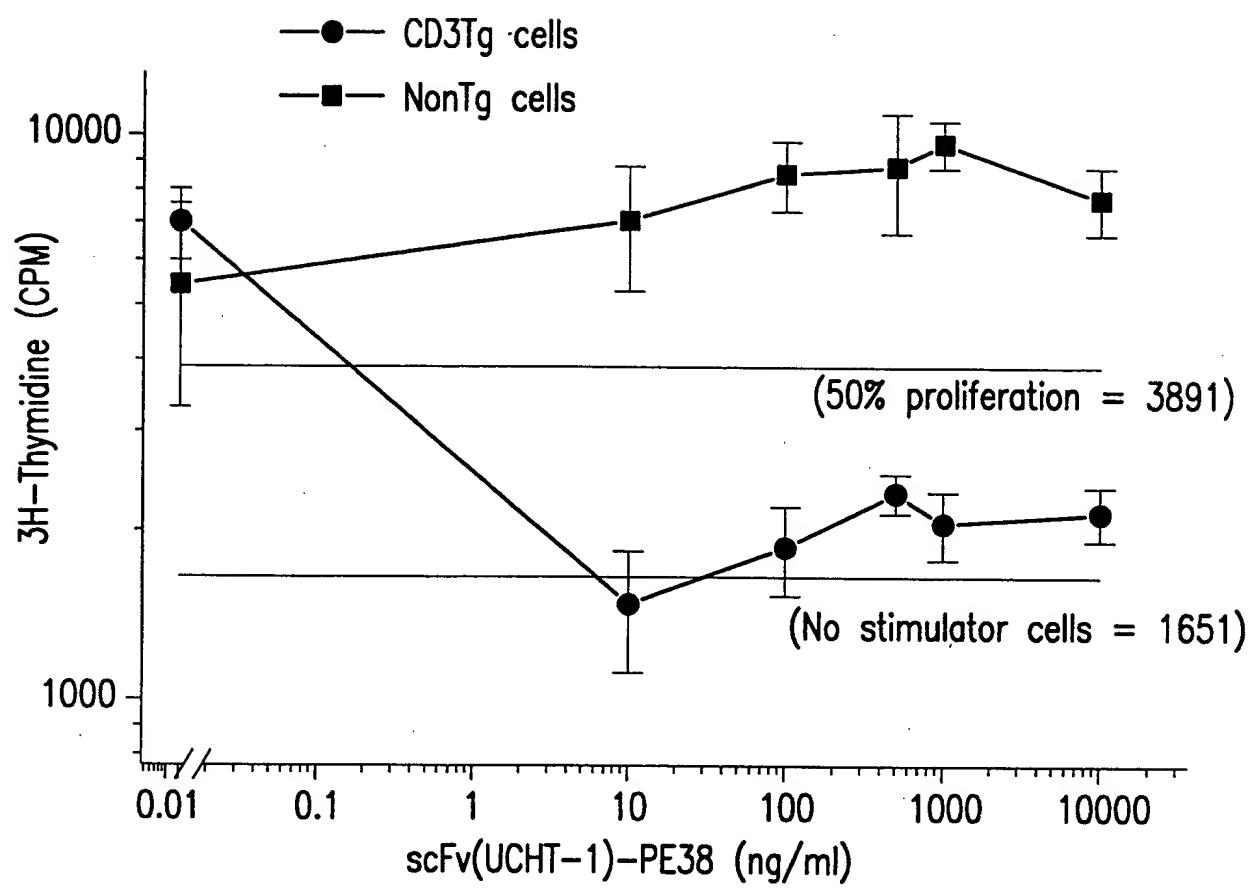


FIG. 9A

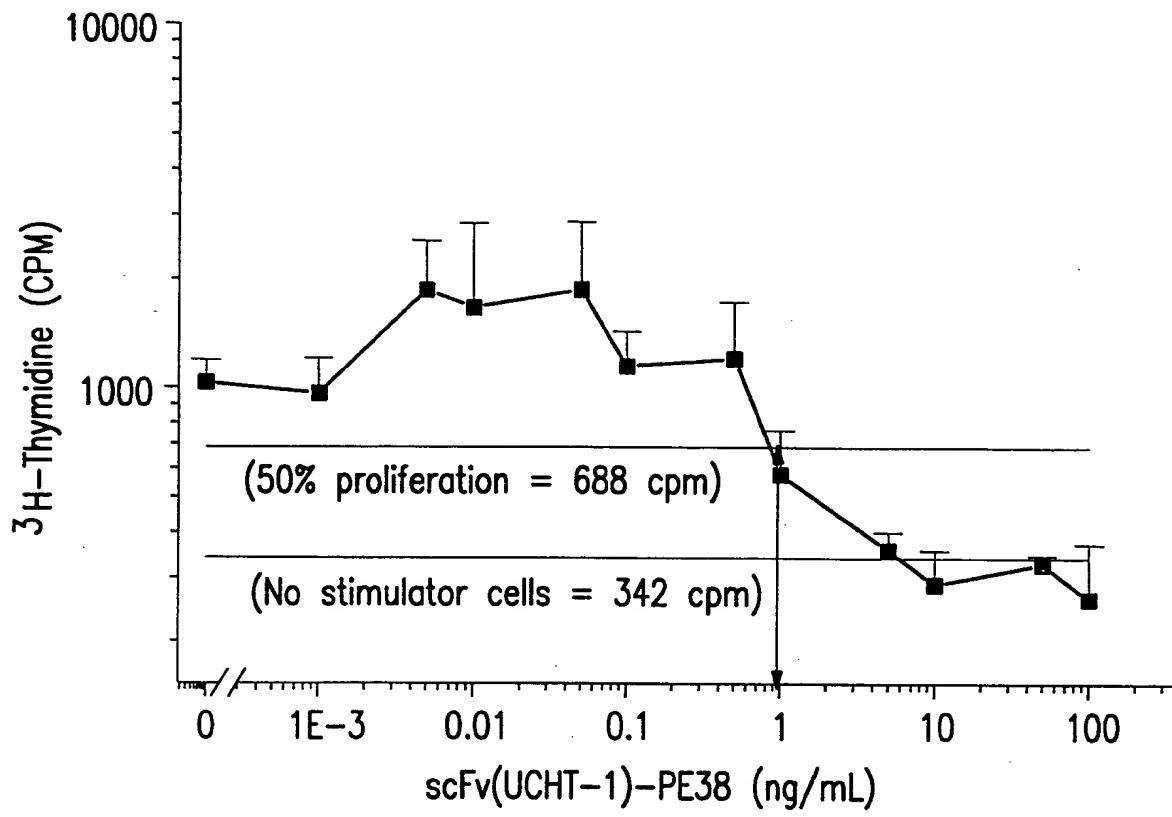


FIG. 9B

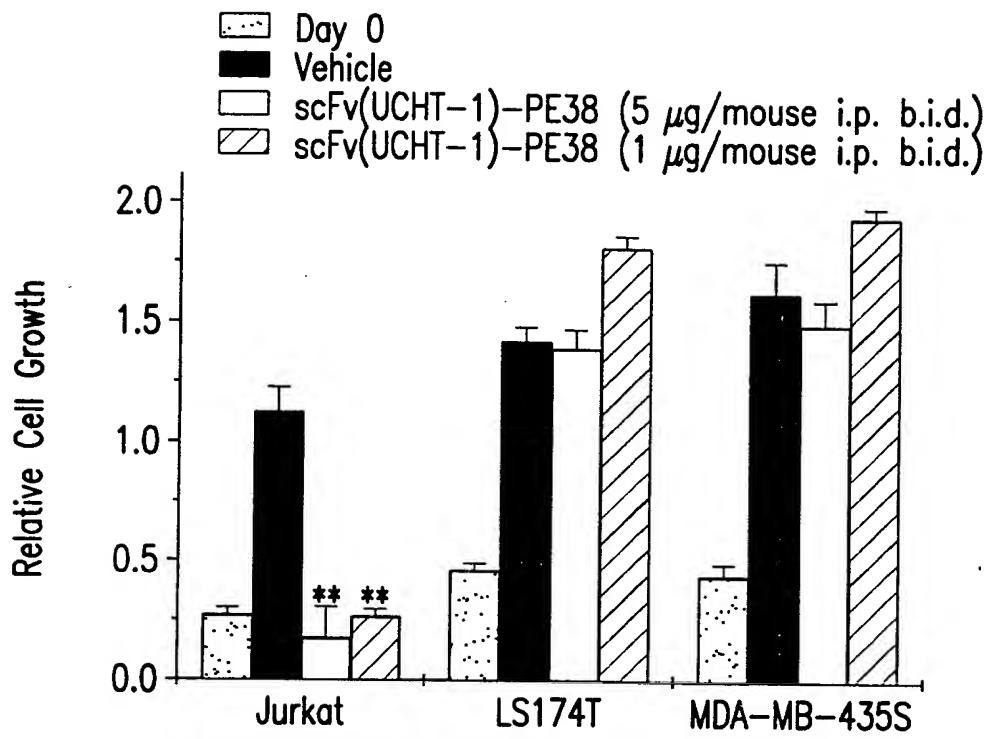


FIG.10

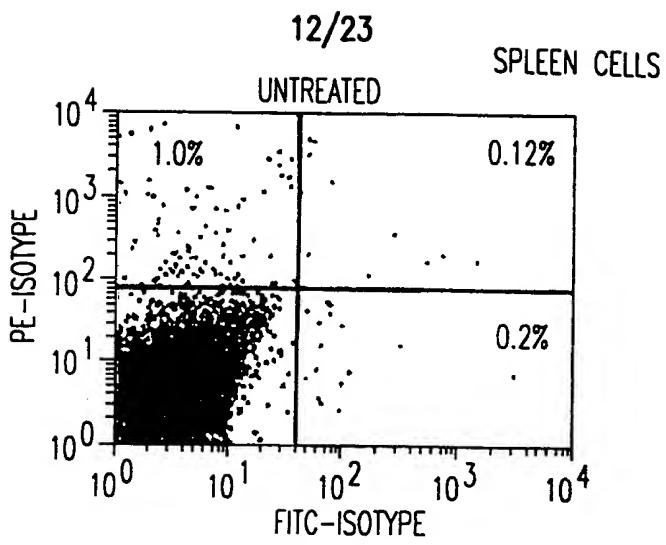


FIG. 11A

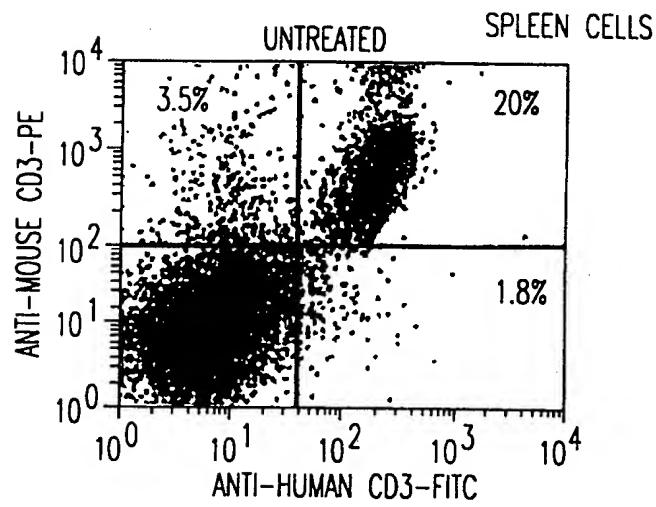


FIG. 11B

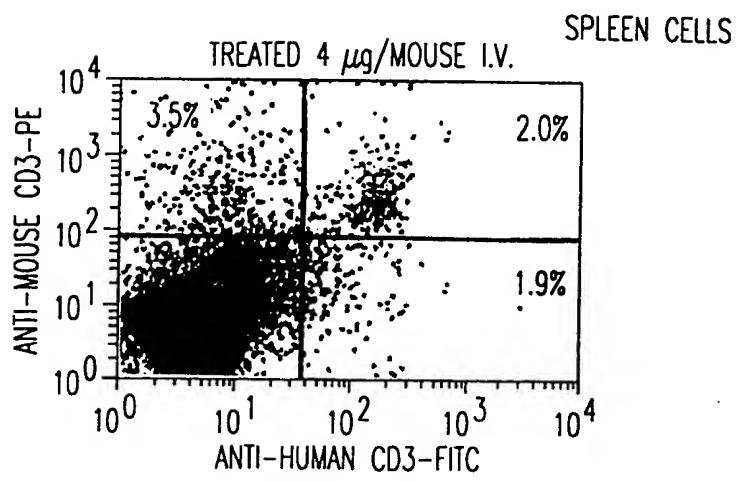


FIG. 11C

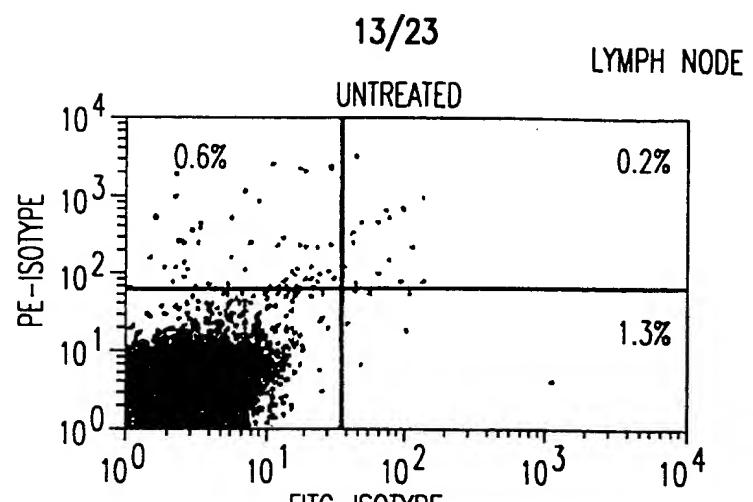


FIG. 12A

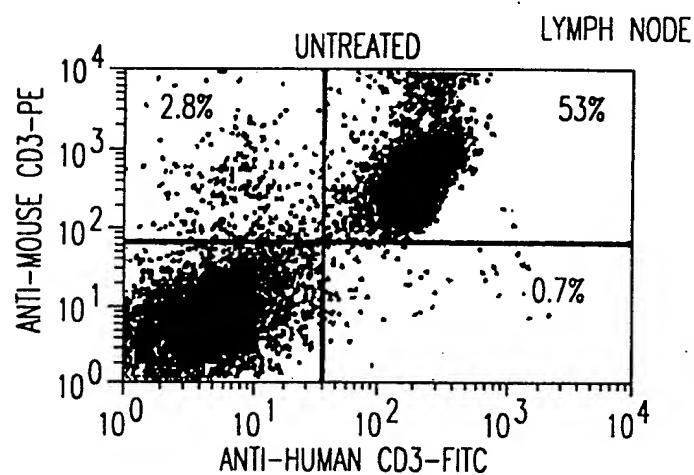


FIG. 12B

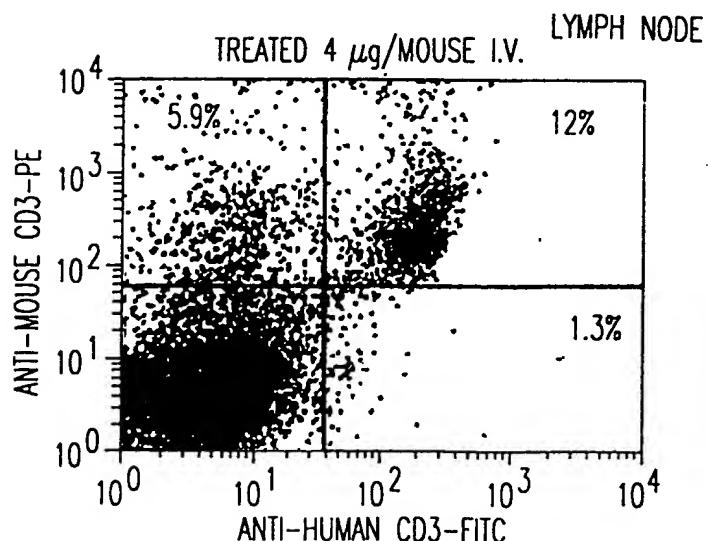


FIG. 12C

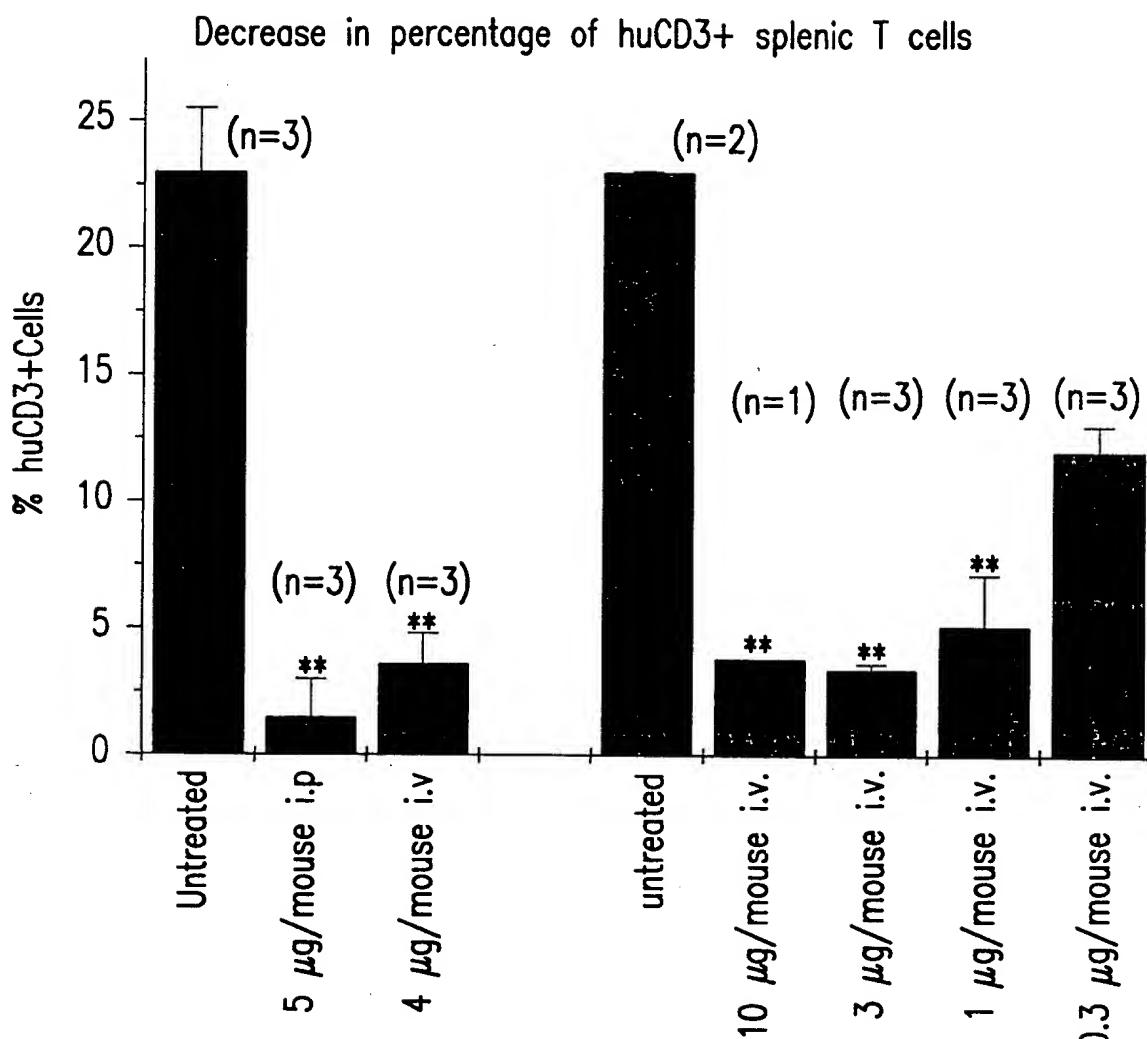


FIG. 13A

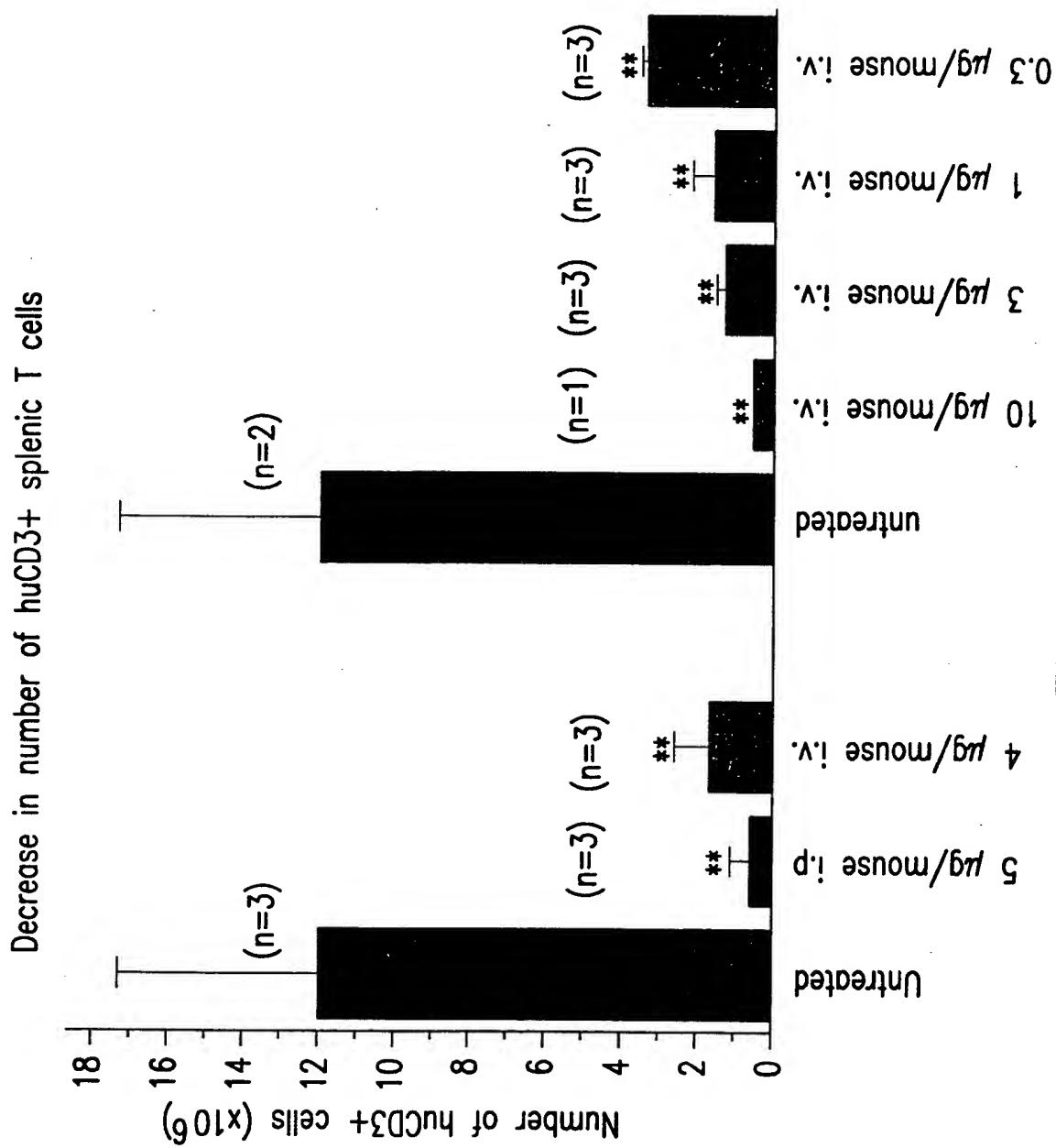


FIG. 13B

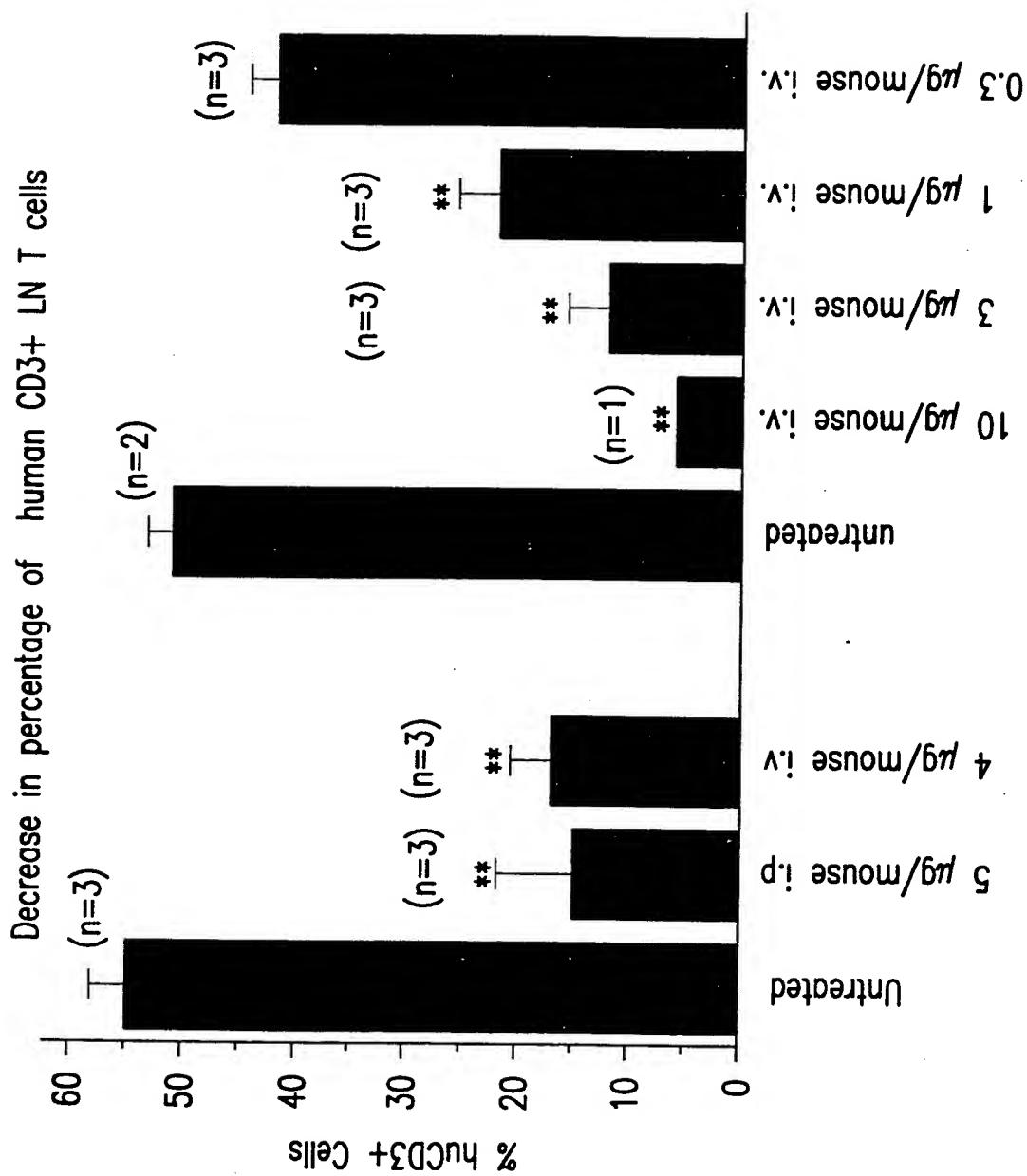


FIG. 14A

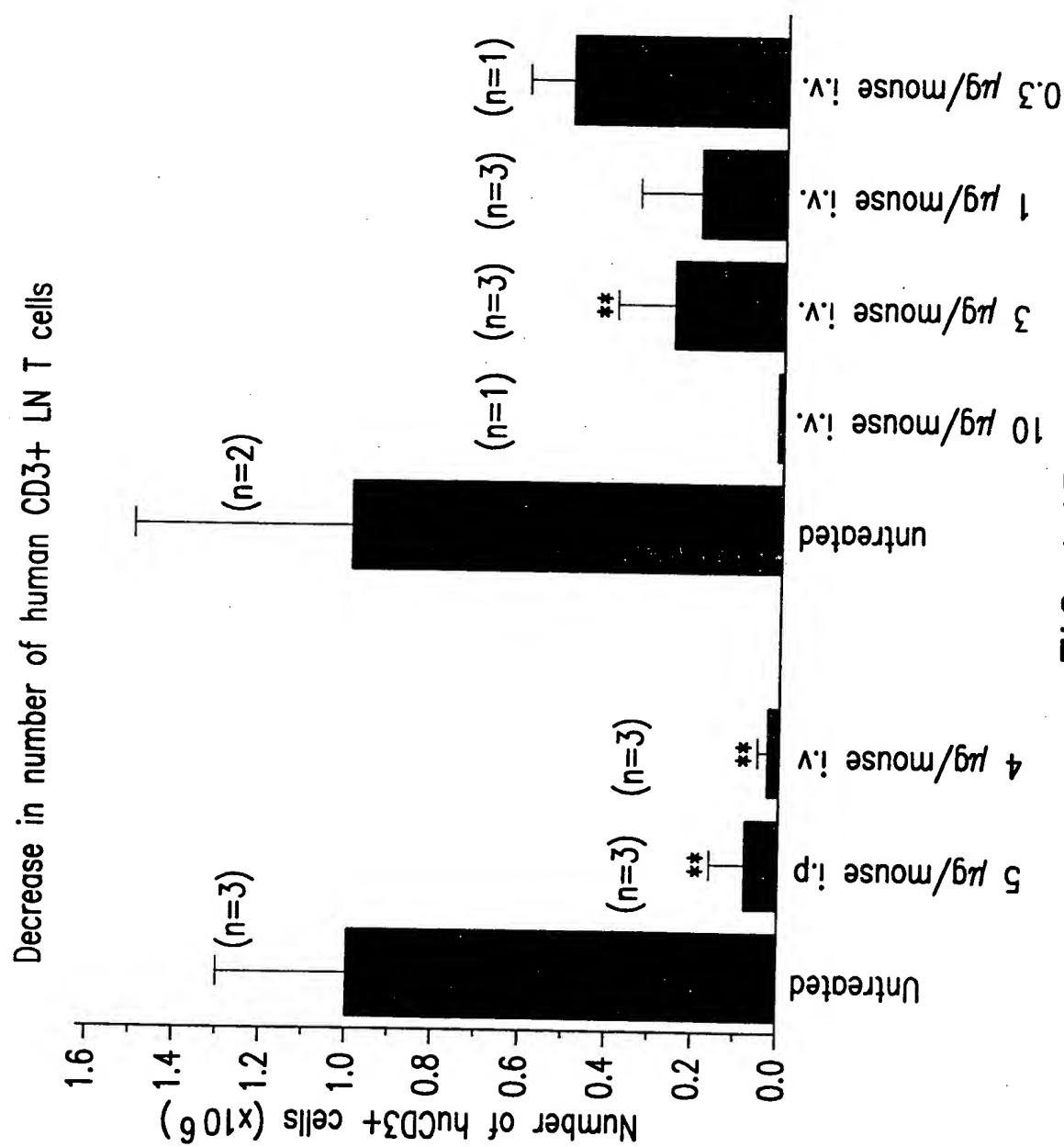


FIG. 14B

## Nucleotide and amino acid sequence of scFv(UCHT-1)-PE38

1 CCATGGCGGACATCCAGATGACCCAGACCACCTCCTCCCTGTCTGCCTCTGGGAGACA 60  
M A D I Q M T Q T T S S L S A S L G D R

61 GAGTCACCACAGTTGCAGGGCAAGTCAGGACATTAGAAATTATTAACCTGGTATCAAC 120  
V T I S C R A S Q D I R N Y L N W Y Q Q

121 AGAAACCAGATGGAACGTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAG 180  
K P D G T V K L L I Y Y T S R L H S G V

181 TCCCCATCAAAGTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATAGCAACC 240  
P S K F S G S G S G T D Y S L T I S N L

241 TGGACCAAGAGGATATTGCCACTTACTTTGCCAACAGGTAATACGCTTCCGTGGACGT 300  
E Q E D I A T Y F C Q Q G N T L P W T F

301 TCGCTGGAGGCACCAAGCTGAAATCAAACGGGCTGGAGGGCGTAGTGGCGGTGGATCGG 360  
A G G T K L E I K R A G G G S G G G S G

361 GTGGAGGCAGCGGTGGCGATCTGAGGTCCAGCTCCAGCAGTCTGGACCTGAGCTGGTGA 420  
G G S G G G S E V Q L Q Q S G P E L V K

421 AGCCTGGAGCTTCAATGAAGATATCCTGAAAGCTTCTGGTACTCATTCACTGGCTACA 480  
P G A S M K I S C K A S G Y S F T G Y T

481 CCATGAACTGGTGAAGCAGAGTCATGAAAGAACCTTGACTGGATGGACTTATTAATC 540  
M N W V K Q S H G K N L E W M G L I N P

541 CTTACAAAGCTTACCTACAACCAGAAGTTCAAGGACAAGGCCACATTAACGTGAG 600  
Y K G V S T Y N Q K F K D K A T L T V D

601 ACAACTCATCCAGCACGCCACATGAAACTCCTCAGTCTGACATCTGAGGACTCTGCAG 660  
K S S S T A Y M E L L S L T S E D S A V

661 TCTATTACTGTCAAGATCGGGTACTACGGTGTAGTCACTGGTACTTCGATGTCTGG 720  
Y Y C A R S G Y Y G D S D W Y F D V W G

721 GCGCAGGGACCACGGTCACCGTCTCCTCAAAGCTTCCCGAGGTCCCAGGGCGCAGCC 780  
A G T T V T V S S K A S G G P E G G S L

781 TGGCCCCGCTGACCCGGCACCAAGGCTTGGCACCTGGGAGACTTCAACCGTCATC 840  
A A L T A H Q A C H L P L E T F T R H R

FIG. 15A

841 GCCAGCCGCCGGCTGGAAACAACCTGGAGCAGTGGCGTATCCGTGCAGCGGCTGGTCG 900  
     Q P R G W E Q L E Q C G Y P V Q R L V A  
  
 901 CCCTCTACCTGGCGCGCGCTCTCGTGGAAACCAGGTGACCAAGGTGATCCGCAACGCC 960  
     L Y L A A R L S W N Q V D Q V I R N A L  
  
 961 TGGCCAGCCCCGGCACCGGCGGACCTGGCGAAGCGATCCGGACCAGGGAGCAGGGAGCAGG 1020  
     A S P G S G G D L G E A I R E Q P E Q A  
  
 1021 CCCGTCTGGCCCTGACCCCTGGCCGCCGGAGACGGAGCCCTCGTCCGGCAGGGCACCG 1080  
     R L A L T L A A A E S E R F V R Q G T G  
  
 1081 GCAACGACGAGGCCGGCGCCCAACGCCGGGACACGCCGACGCCCTGCTGGAGC 1140  
     N D E A G A A N G P A D S G D A L L E R  
  
 1141 GCAACTATCCCCTGGCGGGAGTTCCCTGGGACGGGGGACCTCAGCTTCAGCACCC 1200  
     N Y P T G A E F L G D G G D V S F S T R  
  
 1201 GCGGCACCGAGAACTGGACGGTGAGCGGCTGCTCCAGGGCACCGCAACTGGAGGAGC 1260  
     G T Q N W T V E R L L Q A H R Q L E E R  
  
 1261 GCGGCTATGTGTCGCGCTACACGGCACCTTCCTCGAACGGGCAAACCATCGTCT 1320  
     G Y V F V G Y H G T F L E A A Q S I V F  
  
 1321 TCGCCGGCTGCGCGCCAGCCAGGACCTCGACGGATCTGGCGGTTCTATATCG 1380  
     G G V R A R S Q D L D A I W R G F Y I A  
  
 1381 CGGGCGATCCGGCGCTGGCTACGGCTACGCCAGGACCGAACCCACGCACGCC 1440  
     G D P A L A Y G Y A Q D Q E P D A R G R  
  
 1441 GGATCCGCAACGGTGCCTGCTGGGGTCTATGTGCCCGCTCGAGGCTGCCGGCTCT 1500  
     I R N G A L L R V Y V P R S S L P G F Y  
  
 1501 ACCGCACCGCCTGACCCCTGGCCGCCGGAGGGGGGGGGAGGTGCAACGGCTGATCG 1560  
     R T S L T L A A P E A A G E V E R L I G  
  
 1561 GCCATCCGCTGCCCTGCGCCTGGACGCCATCACGGGGGGGGAGGAGGAAGGGGGGCC 1620  
     H P L P L R L D A I T G P E E E G G R L  
  
 1621 TCGAGACCAATTCTCCGCTGGCCCTGGCCGAGGGCACCGTGGTATTCCCTGGGATCC 1680  
     E T I L G W P L A E R T V V I P S A I P

1681 CCACCGACCCGGCAACGTGGGGGACCTCGACCCGTCCAGCATCCCCACAAGAAC 1740  
T D P R N V G G D L D P S S I P D K E Q

1741 AGCCGATCAGGCCCTGCCGGACTACGCCAGCCAGCCCAAACCGCCGCCGAGGACC 1800  
A I S A L P D Y A S Q P G K P P R E D L

1801 TGAAGTAAC TGCCGCCACCGCCGGCTCCCTCGCAGGAGCCGGCCTCTCGGGCTGG 1860  
K \*

1861 CCATACATCAGTTCTGATGCCAGCCAATCGAATATGAATTCTCGAGACGTACGG 1920

1921 TCGCGCCGATGCATTCAAGATCC 1944

FIG. 15C

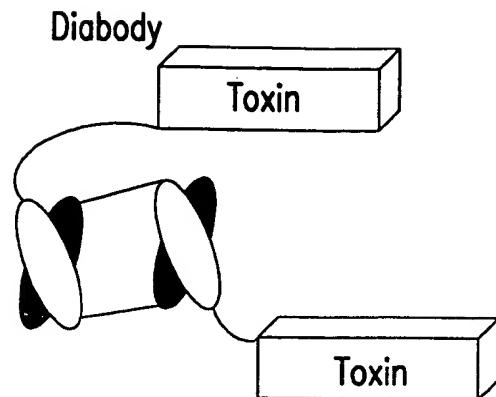


FIG. 16A

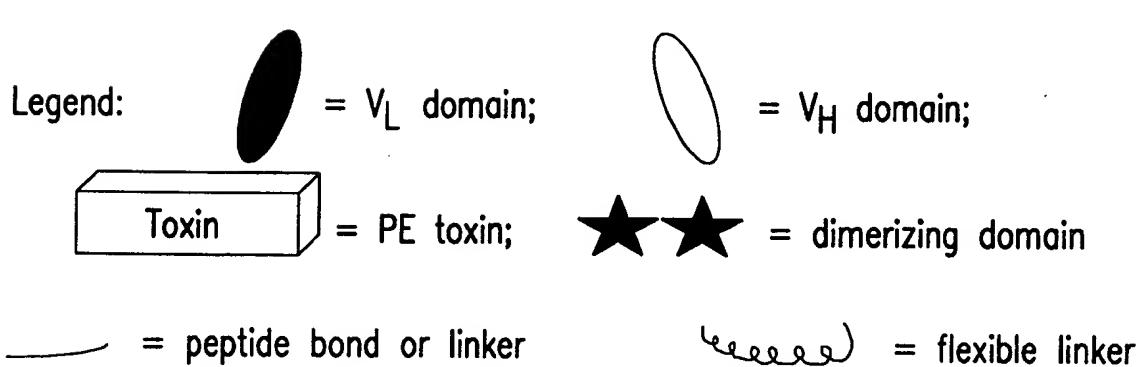
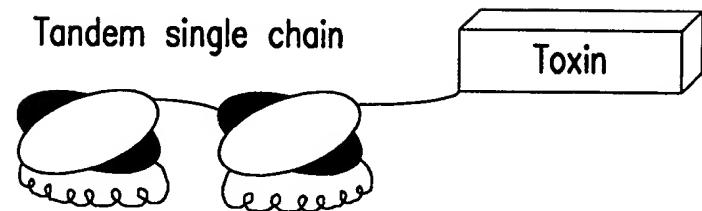


FIG. 16B

Dimerizing domains

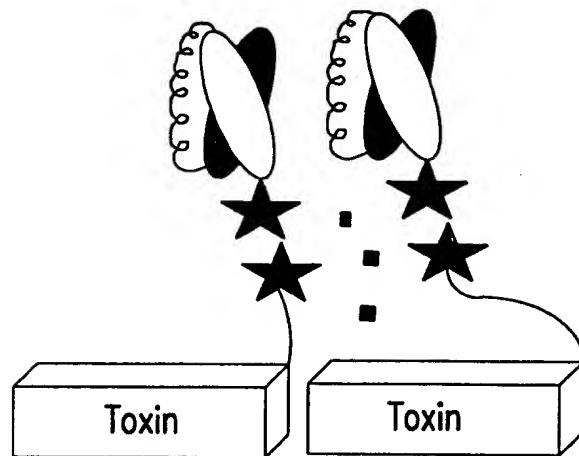


FIG. 16C

"Minibody" -toxin /  $\Delta$  minibody -toxin

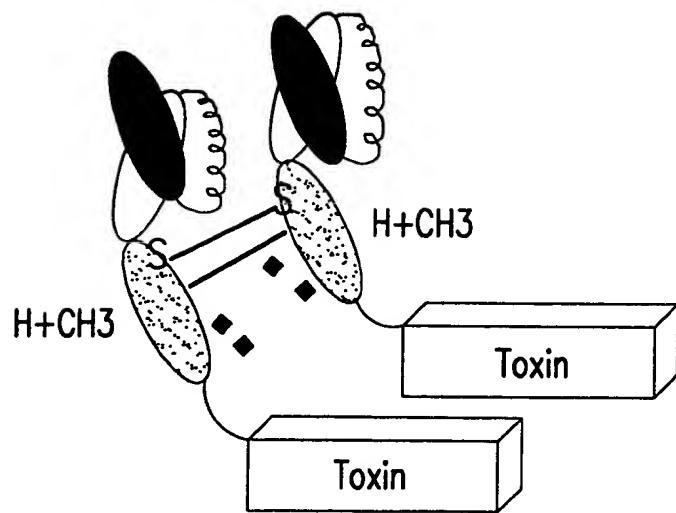


FIG. 16D

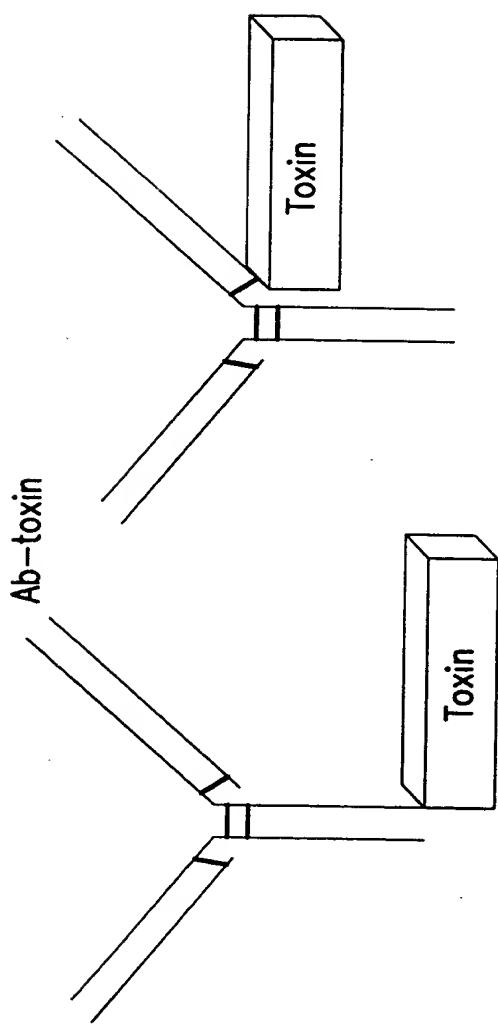


FIG. 16E

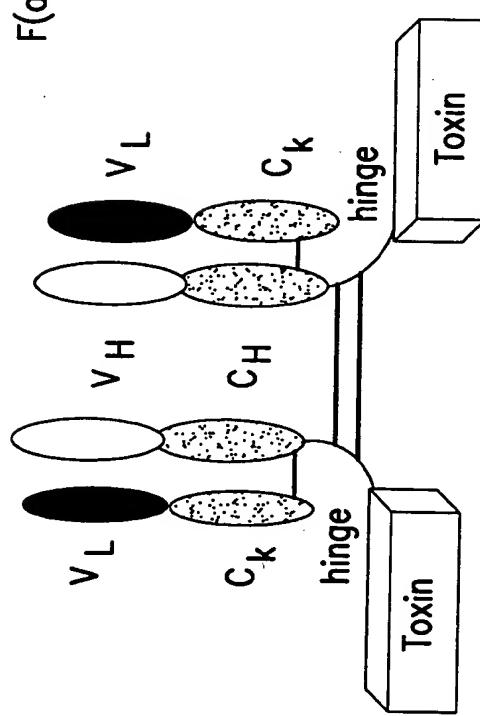
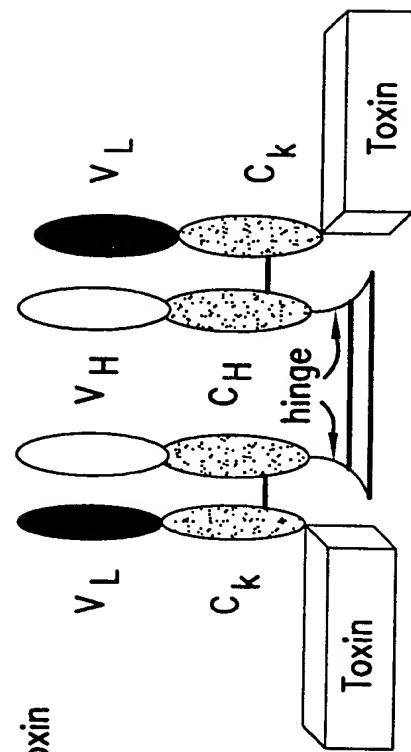


FIG. 16F